What is claimed:

1. A method of identifying a nucleic acid molecule associated with a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1; and

b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a nucleic acid molecule associated with a cardiovascular or tumorigenic disorder.

2. The method of claim 1, wherein said hybridization probe is detectably labeled.

3. The method of claim 1, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

4. The method of claim 1, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

5. The method of claim 1, wherein said detecting is by *in situ* hybridization.

6. A method of identifying a nucleic acid associated with a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1;

b) incubating said sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a nucleic acid molecule associated with a cardiovascular or tumorigenic disorder.

7. The method of claim 6, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

8. The method of any one of claims 1 or 6, wherein said method is used to detect mRNA in said sample.

9. The method of any one of claims 1 or 6, wherein said method is used to detect genomic DNA in said sample.

10. A method of identifying a polypeptide associated with a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample comprising polypeptides with a GPCR 4941 binding substance; and

b) detecting the presence of a polypeptide in said sample that binds to said GPCR 4941 binding substance, thereby identifying a polypeptide associated with a cardiovascular or tumorigenic disorder.

11. The method of claim 10, wherein said binding substance is an antibody.

12. The method of claim 10, wherein said binding substance is detectably labeled.

13. A method of identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1; and

b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder.

14. The method of claim 13, wherein said hybridization probe is detectably labeled.

15. The method of claim 13, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

16. The method of claim 13, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

17. The method of claim 13, wherein said detecting is by *in situ* hybridization.

18. A method of identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1;

b) incubating said sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder.

19. The method of claim 18, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

20. The method of any one of claims 13 or 18, wherein said method is used to detect mRNA in said sample.

21. The method of any one of claims 13 or 18, wherein said method is used to detect genomic DNA in said sample.

22. A method of identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder comprising:

a) contacting a sample obtained from said subject comprising polypeptides with a GPCR 4941 binding substance; and

b) detecting the presence of a polypeptide in said sample that binds to said GPCR 4941 binding substance, thereby identifying a subject having a cardiovascular or tumorigenic disorder, or at risk for developing a cardiovascular or tumorigenic disorder.

23. The method of claim 22, wherein said binding substance is an antibody.

24. The method of claim 22, wherein said binding substance is detectably labeled.

25. A method for identifying a compound capable of treating a cardiovascular or tumorigenic disorder characterized by aberrant GPCR 4941 nucleic acid expression or GPCR 4941 polypeptide activity comprising assaying the ability of the compound to modulate GPCR 4941 nucleic acid expression or GPCR 4941 polypeptide activity, thereby identifying a compound capable of treating a cardiovascular or tumorigenic disorder characterized by aberrant GPCR 4941 nucleic acid expression or GPCR 4941 polypeptide activity.

26. The method of claim 25, wherein the disorder a disorder associated with aberrant angiogenesis.

27. The method of claim 25, wherein the disorder is a disorder associated with aberrant vascularization.

28. The method of claim 25, wherein the disorder is atherosclerosis.

29. The method of claim 25, wherein the disorder is ovarian cancer.

30. The method of claim 25, wherein the ability of the compound to modulate the activity of the GPCR 4941 polypeptide is determined by detecting the induction of an intracellular second messenger.

31. A method for treating a subject having a cardiovascular or tumorigenic disorder characterized by aberrant GPCR 4941 polypeptide activity or aberrant GPCR 4941 nucleic acid expression comprising administering to the subject a GPCR 4941 modulator, thereby treating said subject having a cardiovascular or tumorigenic disorder.

32. The method of claim 31, wherein the GPCR 4941 modulator is a small molecule.

33. The method of claim 31, wherein the disorder is a disorder associated with aberrant angiogenesis.

34. The method of claim 31, wherein the disorder is a disorder associated with aberrant vascularization.

35. The method of claim 31, wherein the disorder is atherosclerosis.

36. The method of claim 31, wherein the disorder is ovarian cancer.

37. The method of claim 31, wherein said GPCR 4941 modulator is administered in a pharmaceutically acceptable formulation.

38. The method of claim 31, wherein said GPCR 4941 modulator is administered using a gene therapy vector.

39. The method of 31, wherein the GPCR 4941 modulator is capable of modulating GPCR 4941 polypeptide activity.

40. The method of claim 39, wherein the GPCR 4941 modulator is an anti-GPCR 4941 antibody.

41. The method of claim 39, wherein the GPCR 4941 modulator is a GPCR 4941 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

42. The method of claim 39, wherein the GPCR 4941 modulator is a GPCR 4941 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, wherein said percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4.

43. The method of claim 39, wherein the GPCR 4941 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 at 4X SSC at 65-70°C followed by one or more washes in 1X SSC, at 65-70°C.

44. The method of claim 31, wherein the GPCR 4941 modulator is capable of modulating GPCR 4941 nucleic acid expression.

45. The method of claim 44, wherein the GPCR 4941 modulator is an antisense GPCR 4941 nucleic acid molecule.

46. The method of claim 44, wherein the GPCR 4941 modulator is a ribozyme.

47. The method of claim 44, wherein the GPCR 4941 modulator comprises the nucleotide sequence of SEQ ID NO:1, or a fragment thereof.

48. The method of claim 44, wherein the GPCR 4941 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, wherein said percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4.

49. The method of claim 44, wherein the GPCR 4941 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 at 4X SSC at 65-70°C followed by one or more washes in 1X SSC, at 65-70°C.

50. A method for identifying a compound capable of modulating an endothelial cell activity comprising:

a) contacting an endothelial cell with a test compound; and

b) assaying the ability of the test compound to modulate the expression of a GPCR 4941 nucleic acid or the activity of a GPCR 4941 polypeptide;

thereby identifying a compound capable of modulating an endothelial cell activity.

51. The method of claim 50, wherein said endothelial cell activity is cell proliferation.

52. The method of claim 50, wherein said endothelial cell activity is cell migration.

53. The method of claim 50, wherein said endothelial cell activity is expression of cell surface adhesion molecules.

54. A method for modulating an endothelial cell activity comprising contacting an endothelial cell with a GPCR 4941 modulator, thereby modulating said endothelial cell activity.

55. The method of claim 54, wherein the GPCR 4941 modulator is a small molecule.

56. The method of claim 54, wherein said endothelial cell activity is cell proliferation.

57. The method of claim 54, wherein said endothelial cell activity is cell migration.

58. The method of claim 54, wherein said endothelial cell activity is expression of cell surface adhesion molecules.

59. The method of claim 54, wherein the GPCR 4941 modulator is capable of modulating GPCR 4941 polypeptide activity.

60. The method of claim 59, wherein the GPCR 4941 modulator is an anti-GPCR 4941 antibody.

61. The method of claim 59, wherein the GPCR 4941 modulator is a GPCR 4941 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

62. The method of claim 59, wherein the GPCR 4941 modulator is a GPCR 4941 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, wherein said percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4.

63. The method of claim 59, wherein the GPCR 4941 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 at 4X SSC at 65-70°C followed by one or more washes in 1X SSC, at 65-70°C.

64. The method of claim 54, wherein the GPCR 4941 modulator is capable of modulating GPCR 4941 nucleic acid expression.

65. The method of claim 64, wherein the GPCR 4941 modulator is an antisense GPCR 4941 nucleic acid molecule.

66. The method of claim 64, wherein the GPCR 4941 modulator is a ribozyme.

67. The method of claim 64, wherein the GPCR 4941 modulator comprises the nucleotide sequence of SEQ ID NO:1, or a fragment thereof.

68. The method of claim 64, wherein the GPCR 4941 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, wherein said percent identity is calculated using the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4.

69. The method of claim 64, wherein the GPCR 4941 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 at 4X SSC at 65-70°C followed by one or more washes in 1X SSC, at 65-70°C.